



1

SEQUENCE LISTING

<110> ULLRICH, AXEL
GISHIZKY, MIKHAIL
SURES, IRMINGARD

<120> NOVEL MEGAKARYOCYTIC PROTEIN TYROSINE KINASES

<130> 038602/1259

<140> 09/977,261
<141> 2001-10-16

<150> 08/232,545
<151> 1994-04-22

<160> 24

<170> PatentIn Ver. 2.1

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<211> 2000
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<222> (258) .. (1778)

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kinase 1

a¹⁴

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aggctcggtc cagtgccacc cagctcccta cctcctgtgc cagccgcctg gcctgtggca 180
ggccattcccc acgtcccccg actgtgacca ctggctcagt gtgcctctca cctgcctcag 240
tttccctctg gggggcg atg gcg ggg cga ggc tct ctg gtt tcc tgg cgg 290
Met Ala Gly Arg Gly Ser Leu Val Ser Trp Arg
1 5 10

gca ttt cac ggc tgt gat tct gct gag gaa ctt ccc cgg gtg agc ccc 338
Ala Phe His Gly Asp Ser Ala Glu Glu Leu Pro Arg Val Ser Pro
15 20 25

cgc ttc ctc cga gcc tgg cac ccc cct ccc gtc tca gcc agg atg cca 386
Arg Phe Leu Arg Ala Trp His Pro Pro Pro Val Ser Ala Arg Met Pro
30 35 40

acg agg cgc tgg gcc ccg ggc acc cag tgt atc acc aaa tgc gag cac 434
Thr Arg Arg Trp Ala Pro Gly Thr Gln Cys Ile Thr Lys Cys Glu His
45 50 55

acc cgc ccc aag cca ggg gag ctg gcc ttc cgc aag ggc gac gtg gtc		482	
Thr Arg Pro Lys Pro Gly Glu Leu Ala Phe Arg Lys Gly Asp Val Val			
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acc atc ctg gag gcc tgc gag aac aag agc tgg tac cgc gtc aag cac		530	
Thr Ile Leu Glu Ala Cys Glu Asn Lys Ser Trp Tyr Arg Val Lys His			
80	85	90	
cac acc agt gga cag gag ggg ctg ctg gca gct ggg gcg ctg cgg gag		578	
His Thr Ser Gly Gln Glu Gly Leu Leu Ala Ala Gly Ala Leu Arg Glu			
95	100	105	
cg _g gag gcc ctc tcc gca gac ccc aag ctc agc ctc atg cc _g tgg tt _c		626	
Arg Glu Ala Leu Ser Ala Asp Pro Lys Leu Ser Leu Met Pro Trp Phe			
110	115	120	
cac ggg aag atc tcg ggc cag gag gct gtc cag cag ctg cag cct ccc		674	
His Gly Lys Ile Ser Gly Gln Glu Ala Val Gln Gln Leu Gln Pro Pro			
125	130	135	
gag gat ggg ctg ttc ctg gtg cg _g gag tcc g _g c _g c _g c _g c _g c _g gac		722	
Glu Asp Gly Leu Phe Leu Val Arg Glu Ser Ala Arg His Pro Gly Asp			
140	145	150	155
tac gtc ctg tgc gtg agc ttt ggc cgc gac gtc atc cac tac cgc gtg		770	
Tyr Val Leu Cys Val Ser Phe Gly Arg Asp Val Ile His Tyr Arg Val			
160	165	170	
ctg cac cgc gac ggc cac ctc aca atc gat gag gcc gtg ttc ttc tgc		818	
Leu His Arg Asp Gly His Leu Thr Ile Asp Glu Ala Val Phe Phe Cys			
175	180	185	
aac ctc atg gac atg gtg gag cat tac agc aag gac aag ggc gct atc		866	
Asn Leu Met Asp Met Val Glu His Tyr Ser Lys Asp Lys Gly Ala Ile			
190	195	200	
tgc acc aag ctg gtg aga cca aag cgg aaa cac ggg acc aag tcg gcc		914	
Cys Thr Lys Leu Val Arg Pro Lys Arg Lys His Gly Thr Lys Ser Ala			
205	210	215	
gag gag gag ctg gcc agg gc _g ggc tgg tta ctg aac ctg cag cat tt _g		962	
Glu Glu Glu Leu Ala Arg Ala Gly Trp Leu Leu Asn Leu Gln His Leu			
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aca ttg gga gca cag atc gga gag gga gag ttt gga gct gtc ctg cag		1010	
Thr Leu Gly Ala Gln Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln			
240	245	250	
ggt gag tac ctg ggg caa aag gtg gcc gtg aag aat atc aag tgt gat		1058	
Gly Glu Tyr Leu Gly Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp			
255	260	265	
gtg aca gcc cag gcc ttc ctg gac gag acg gcc gtc atg acg aag atg		1106	
Val Thr Ala Gln Ala Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met			
270	275	280	

a¹⁴
cont

caa cac gag aac ctg gtg cgt ctc ctg ggc gtg atc ctg cac cag ggg Gln His Asn Leu Val Arg Leu Leu Gly Val Ile Leu His Gln Gly 285 290 295	1154
ctg tac att gtc atg gag cac gtg agc aag ggc aac ctg gtg aac ttt Leu Tyr Ile Val Met Glu His Val Ser Lys Gly Asn Leu Val Asn Phe 300 305 310 315	1202
ctg cgg acc cgg ggt cga gcc ctc gtg aac acc gct cag ctc ctg cag Leu Arg Thr Arg Gly Arg Ala Leu Val Asn Thr Ala Gln Leu Gln 320 325 330	1250
ttt tct ctg cac gtg gcc gag ggc atg gag tac ctg gag agc aag aag Phe Ser Leu His Val Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys 335 340 345	1298
ctt gtg cac cgc gac ctg gcc cgc aac atc ctg gtc tca gag gac Leu Val His Arg Asp Leu Ala Arg Asn Ile Leu Val Ser Glu Asp 350 355 360	1346
ctg gtg gcc aag gtc agc gac ttt ggc ctg gcc aaa gcc gag cgg aag Leu Val Ala Lys Val Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys 365 370 375	1394
ggg cta gac tca agc cgg ctg ccc gtc aag tgg acg gcg ccc gag gct Gly Leu Asp Ser Ser Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala 380 385 390 395	1442
ctc aaa cac ggg aag ttc acc agc aag tcg gat gtc tgg agt ttt ggg Leu Lys His Gly Lys Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly 400 405 410	1490
gtg ctg ctc tgg gag gtc ttc tca tat gga cgg gct ccg tac cct aaa Val Leu Leu Trp Glu Val Phe Ser Tyr Gly Arg Ala Pro Tyr Pro Lys 415 420 425	1538
atg tca ctg aaa gag gtg tcg gag gcc gtg gag aag ggg tac cgc atg Met Ser Leu Lys Glu Val Ser Glu Ala Val Glu Lys Gly Tyr Arg Met 430 435 440	1586
gaa ccc ccc gag ggc tgt cca ggc ccc gtg cac gtc ctc atg agc agc Glu Pro Pro Glu Gly Cys Pro Gly Pro Val His Val Leu Met Ser Ser 445 450 455	1634
tgc tgg gag gca gag ccc gcc cgc cgg cca ccc ttc cgc aaa ctg gcc Cys Trp Glu Ala Glu Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala 460 465 470 475	1682
gag aag ctg gcc cgg gag cta cgc agt gca ggt gcc cca gcc tcc gtc Glu Lys Leu Ala Arg Glu Leu Arg Ser Ala Gly Ala Pro Ala Ser Val 480 485 490	1730
tca ggg cag gac gcc gac ggc tcc acc tcg ccc cga agc cag gag ccc Ser Gly Gln Asp Ala Asp Gly Ser Thr Ser Pro Arg Ser Gln Glu Pro 495 500 505	1778
tgacccacc cgggtggggcc cttggccca gaggaccgag agagtggaga gtgcggcgtg 1838	

ggggcactga ccaggcccaa ggagggtcca ggcccccaag tcatcctcct ggtgcccaca 1898
 gcaggggctg gcccacgtag gggctctgg gccccccgtg gacaccccaag acctgcgaag 1958
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 Trp His Pro Pro Pro Val Ser Ala Arg Met Pro Thr Arg Arg Trp Ala
 35 40 45
 Pro Gly Thr Gln Cys Ile Thr Lys Cys Glu His Thr Arg Pro Lys Pro
 50 55 60
 Gly Glu Leu Ala Phe Arg Lys Gly Asp Val Val Thr Ile Leu Glu Ala
 65 70 75 80
 Cys Glu Asn Lys Ser Trp Tyr Arg Val Lys His His Thr Ser Gly Gln
 85 90 95
 Glu Gly Leu Leu Ala Ala Gly Ala Leu Arg Glu Arg Glu Ala Leu Ser
 100 105 110
 Ala Asp Pro Lys Leu Ser Leu Met Pro Trp Phe His Gly Lys Ile Ser
 115 120 125
 Gly Gln Glu Ala Val Gln Gln Leu Gln Pro Pro Glu Asp Gly Leu Phe
 130 135 140
 Leu Val Arg Glu Ser Ala Arg His Pro Gly Asp Tyr Val Leu Cys Val
 145 150 155 160
 Ser Phe Gly Arg Asp Val Ile His Tyr Arg Val Leu His Arg Asp Gly
 165 170 175
 His Leu Thr Ile Asp Glu Ala Val Phe Phe Cys Asn Leu Met Asp Met
 180 185 190
 Val Glu His Tyr Ser Lys Asp Lys Gly Ala Ile Cys Thr Lys Leu Val
 195 200 205
 Arg Pro Lys Arg Lys His Gly Thr Lys Ser Ala Glu Glu Glu Leu Ala
 210 215 220

Arg Ala Gly Trp Leu Leu Asn Leu Gln His Leu Thr Leu Gly Ala Gln
 225 230 235 240
 Ile Gly Glu Gly Glu Phe Gly Ala Val Leu Gln Gly Glu Tyr Leu Gly
 245 250 255
 Gln Lys Val Ala Val Lys Asn Ile Lys Cys Asp Val Thr Ala Gln Ala
 260 265 270
 Phe Leu Asp Glu Thr Ala Val Met Thr Lys Met Gln His Glu Asn Leu
 275 280 285
 Val Arg Leu Leu Gly Val Ile Leu His Gln Gly Leu Tyr Ile Val Met
 290 295 300
 Glu His Val Ser Lys Gly Asn Leu Val Asn Phe Leu Arg Thr Arg Gly
 305 310 315 320
 Arg Ala Leu Val Asn Thr Ala Gln Leu Leu Gln Phe Ser Leu His Val
 325 330 335
 Ala Glu Gly Met Glu Tyr Leu Glu Ser Lys Lys Leu Val His Arg Asp
 340 345 350
 Leu Ala Ala Arg Asn Ile Leu Val Ser Glu Asp Leu Val Ala Lys Val
 355 360 365
 Ser Asp Phe Gly Leu Ala Lys Ala Glu Arg Lys Gly Leu Asp Ser Ser
 370 375 380
 Arg Leu Pro Val Lys Trp Thr Ala Pro Glu Ala Leu Lys His Gly Lys
 385 390 395 400
 Phe Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu
 405 410 415
 Val Phe Ser Tyr Gly Arg Ala Pro Tyr Pro Lys Met Ser Leu Lys Glu
 420 425 430
 Val Ser Glu Ala Val Glu Lys Gly Tyr Arg Met Glu Pro Pro Glu Gly
 435 440 445
 Cys Pro Gly Pro Val His Val Leu Met Ser Ser Cys Trp Glu Ala Glu
 450 455 460
 Pro Ala Arg Arg Pro Pro Phe Arg Lys Leu Ala Glu Lys Leu Ala Arg
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			Met	Asp	Thr	Lys	Ser	Ile	Leu	Glu	Glu	Leu	
			1					5				10	

ctt	ctc	aaa	aga	tca	cag	caa	aag	aag	aaa	atg	tca	cca	aat	aat	tac	159
Leu	Leu	Lys	Arg	Ser	Gln	Gln	Lys	Lys	Lys	Met	Ser	Pro	Asn	Asn	Tyr	
15							20						25			

aaa	gaa	cg	ctt	ttt	gtt	ttg	acc	aaa	aca	aac	ctt	tcc	tac	tat	gaa	207
Lys	Glu	Arg	Leu	Phe	Val	Leu	Thr	Lys	Thr	Asn	Leu	Ser	Tyr	Tyr	Glu	
30							35					40				

tat	gac	aaa	atg	aaa	agg	ggc	agc	aga	aaa	gga	tcc	att	gaa	att	aag	255
Tyr	Asp	Lys	Met	Lys	Arg	Gly	Ser	Arg	Lys	Gly	Ser	Ile	Glu	Ile	Lys	
45							50					55				

aaa	atc	aga	tgt	gtg	gag	aaa	gta	aat	ctc	gag	gag	cag	acg	cct	gta	303
Lys	Ile	Arg	Cys	Val	Glu	Lys	Val	Asn	Leu	Glu	Glu	Gln	Thr	Pro	Val	
60							65					70				

gag	aga	cag	tac	cca	ttt	cag	att	gtc	tat	aaa	gat	ggg	ctt	ctc	tat	351
Glu	Arg	Gln	Tyr	Pro	Phe	Gln	Ile	Val	Tyr	Lys	Asp	Gly	Leu	Leu	Tyr	
75							80					85			90	

gtc	tat	gca	tca	aat	gaa	gag	agc	cga	agt	cag	tgg	ttg	aaa	gca	tta	399
Val	Tyr	Ala	Ser	Asn	Glu	Glu	Ser	Arg	Ser	Gln	Trp	Leu	Lys	Ala	Leu	
95							100					105				

caa	aaa	gag	ata	agg	ggt	aac	ccc	cac	ctg	ctg	gtc	aag	tac	cat	agt	447
Gln	Lys	Glu	Ile	Arg	Gly	Asn	Pro	His	Leu	Leu	Val	Lys	Tyr	His	Ser	
110							115					120				

ggg	tcc	tcc	gtg	gac	ggg	aag	tcc	ctg	tgt	tgc	cag	cag	agc	tgt	aaa	495
Gly	Phe	Phe	Val	Asp	Gly	Lys	Phe	Leu	Cys	Cys	Gln	Gln	Ser	Cys	Lys	
125							130					135				

gca	gcc	cca	gga	tgt	acc	ctc	tgg	gaa	gca	tat	gct	aat	ctg	cat	act	543
Ala	Ala	Pro	Gly	Cys	Thr	Leu	Trp	Glu	Ala	Tyr	Ala	Asn	Leu	His	Thr	
140							145					150				

gca	gtc	aat	gaa	gag	aaa	cac	aga	gtt	ccc	acc	tcc	cca	gac	aga	gtg	591
Ala	Val	Asn	Glu	Glu	Lys	His	Arg	Val	Pro	Thr	Phe	Pro	Asp	Arg	Val	
155							160					165			170	

ctg aag ata cct cg ^g gca gtt cct gtt ctc aaa atg gat gca cca tct Leu Lys Ile Pro Arg Ala Val Pro Val Leu Lys Met Asp Ala Pro Ser 175	180	185	639	
tca agt acc act cta gcc caa tat gac aac gaa tca aag aaa aac tat Ser Ser Thr Thr Leu Ala Gln Tyr Asp Asn Glu Ser Lys Lys Asn Tyr 190	195	200	687	
ggc tcc cag cca cca tct tca agt acc agt cta gc ^g caa tat gac agc Gly Ser Gln Pro Pro Ser Ser Thr Ser Leu Ala Gln Tyr Asp Ser 205	210	215	735	
aac tca aag aaa atc tat ggc tcc cag cca aac ttc aac atg cag tat Asn Ser Lys Ile Tyr Gly Ser Gln Pro Asn Phe Asn Met Gln Tyr 220	225	230	783	
att cca agg gaa gac ttc cct gac tgg tgg caa gta aga aaa ctg aaa Ile Pro Arg Glu Asp Phe Pro Asp Trp Trp Gln Val Arg Lys Leu Lys 235	240	245	250	831
agt agc agc agc agt gaa gat gtt gca agc agt aac caa aaa gaa aga Ser Ser Ser Ser Glu Asp Val Ala Ser Ser Asn Gln Lys Glu Arg 255	260	265	879	
aat gtg aat cac acc acc tca aag att tca tgg gaa ttc cct gag tca Asn Val Asn His Thr Thr Ser Lys Ile Ser Trp Glu Phe Pro Glu Ser 270	275	280	927	
agt tca tct gaa gaa gag gaa aac ctg gat gat tat gac tgg ttt gct Ser Ser Ser Glu Glu Glu Asn Leu Asp Asp Tyr Asp Trp Phe Ala 285	290	295	975	
gg ^t aac atc tcc aga tca caa tct gaa cag tta ctc aga caa aag gga Gly Asn Ile Ser Arg Ser Gln Ser Glu Gln Leu Leu Arg Gln Lys Gly 300	305	310	1023	
aaa gaa gga gca ttt atg gtt aga aat tcg agc caa gtg gga atg tac Lys Glu Gly Ala Phe Met Val Arg Asn Ser Ser Gln Val Gly Met Tyr 315	320	325	330	1071
aca gtg tcc tta ttt agt aag gct gtg aat gat aaa aaa gga act gtc Thr Val Ser Leu Phe Ser Lys Ala Val Asn Asp Lys Lys Gly Thr Val 335	340	345	1119	
aaa cat tac cac gtg cat aca aat gct gag aac aaa tta tac ctg gca Lys His Tyr His Val His Thr Asn Ala Glu Asn Lys Leu Tyr Leu Ala 350	355	360	1167	
gaa aac tac tgt ttt gat tcc att cca aag ctt att cat tat cat caa Glu Asn Tyr Cys Phe Asp Ser Ile Pro Lys Leu Ile His Tyr His Gln 365	370	375	1215	
cac aat tca gca ggc atg atc aca cg ^g ctc cgc cac cct gtg tca aca His Asn Ser Ala Gly Met Ile Thr Arg Leu Arg His Pro Val Ser Thr 380	385	390	1263	

aag gcc aac aag gtc ccc gac tct gtg tcc ctg gga aat gga atc tgg Lys Ala Asn Lys Val Pro Asp Ser Val Ser Leu Gly Asn Gly Ile Trp 395 400 405 410	1311
gaa ctg aaa aga gaa gag att acc ttg ttg aag gag ctg gga agt ggc Glu Leu Lys Arg Glu Glu Ile Thr Leu Leu Lys Glu Leu Gly Ser Gly 415 420 425	1359
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ttc tat gga gtg tgt tca aag gaa tac ccc ata tac ata gtg act gaa Phe Tyr Gly Val Cys Ser Lys Glu Tyr Pro Ile Tyr Ile Val Thr Glu 475 480 485 490	1551
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tgg gag gtg ttc agc ctg ggg aag cag ccc tat gac ttg tat gac aac Trp Glu Val Phe Ser Leu Gly Lys Gln Pro Tyr Asp Leu Tyr Asp Asn 605 610 615	1935

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Ser Gln Val Val Leu Lys Val Ser Gln Gly His Arg Leu Tyr Arg Pro			
620	625	630	
cac ctg gca tcg gac acc atc tac cag atc atg tac agc tgc tgg cac		2031	
His Leu Ala Ser Asp Thr Ile Tyr Gln Ile Met Tyr Ser Cys Trp His			
635	640	645	650
gag ctt cca gaa aag cgt ccc aca ttt cag caa ctc ctg tct tcc att		2079	
Glu Leu Pro Glu Lys Arg Pro Thr Phe Gln Gln Leu Leu Ser Ser Ile			
655	660	665	
gaa cca ctt cgg gaa aaa gac aag cat tgaagaagaa attaggagtg		2126	
Glu Pro Leu Arg Glu Lys Asp Lys His			
670	675		
ctgataagaa tgaatataga tgctggccag cattttcatt catttaagg aaagtagcaa	2186		
ggcataatgt aatttagcta gttttaata gtgttctctg tattgtctat tatttagaaa	2246		
tgaacaaggc agaaaacaaa agattccctt gaaatttagg tcaaattagt aattttgtt	2306		
atgctgcccc tcatataaca cttccagcc tatagcagaa gcacatttc agactgcaat	2366		
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<212> PRT

<213> Unknown Organism

<220>

<223> Description of Unknown Organism: Megakaryocyte
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35 40 45Gly Ser Arg Lys Gly Ser Ile Glu Ile Lys Lys Ile Arg Cys Val Glu
50 55 60Lys Val Asn Leu Glu Glu Gln Thr Pro Val Glu Arg Gln Tyr Pro Phe
65 70 75 80Gln Ile Val Tyr Lys Asp Gly Leu Leu Tyr Val Tyr Ala Ser Asn Glu
85 90 95

Glu Ser Arg Ser Gln Trp Leu Lys Ala Leu Gln Lys Glu Ile Arg Gly
 100 105 110
 Asn Pro His Leu Leu Val Lys Tyr His Ser Gly Phe Phe Val Asp Gly
 115 120 125
 Lys Phe Leu Cys Cys Gln Gln Ser Cys Lys Ala Ala Pro Gly Cys Thr
 130 135 140
 Leu Trp Glu Ala Tyr Ala Asn Leu His Thr Ala Val Asn Glu Glu Lys
 145 150 155 160
 His Arg Val Pro Thr Phe Pro Asp Arg Val Leu Lys Ile Pro Arg Ala
 165 170 175
 Val Pro Val Leu Lys Met Asp Ala Pro Ser Ser Ser Thr Thr Leu Ala
 180 185 190
 Gln Tyr Asp Asn Glu Ser Lys Lys Asn Tyr Gly Ser Gln Pro Pro Ser
 195 200 205
 Ser Ser Thr Ser Leu Ala Gln Tyr Asp Ser Asn Ser Lys Lys Ile Tyr
 210 215 220
 Gly Ser Gln Pro Asn Phe Asn Met Gln Tyr Ile Pro Arg Glu Asp Phe
 225 230 235 240
 Pro Asp Trp Trp Gln Val Arg Lys Leu Lys Ser Ser Ser Ser Glu
 245 250 255
 Asp Val Ala Ser Ser Asn Gln Lys Glu Arg Asn Val Asn His Thr Thr
 260 265 270
 Ser Lys Ile Ser Trp Glu Phe Pro Glu Ser Ser Ser Glu Glu Glu
 275 280 285
 Glu Asn Leu Asp Asp Tyr Asp Trp Phe Ala Gly Asn Ile Ser Arg Ser
 290 295 300
 Gln Ser Glu Gln Leu Leu Arg Gln Lys Gly Lys Glu Gly Ala Phe Met
 305 310 315 320
 Val Arg Asn Ser Ser Gln Val Gly Met Tyr Thr Val Ser Leu Phe Ser
 325 330 335
 Lys Ala Val Asn Asp Lys Lys Gly Thr Val Lys His Tyr His Val His
 340 345 350
 Thr Asn Ala Glu Asn Lys Leu Tyr Leu Ala Glu Asn Tyr Cys Phe Asp
 355 360 365
 Ser Ile Pro Lys Leu Ile His Tyr His Gln His Asn Ser Ala Gly Met
 370 375 380
 Ile Thr Arg Leu Arg His Pro Val Ser Thr Lys Ala Asn Lys Val Pro
 385 390 395 400

Asp Ser Val Ser Leu Gly Asn Gly Ile Trp Glu Leu Lys Arg Glu Glu
 405 410 415

 Ile Thr Leu Leu Lys Glu Leu Gly Ser Gly Gln Phe Gly Val Val Gln
 420 425 430

 Leu Gly Lys Trp Lys Gly Gln Tyr Asp Val Ala Val Lys Met Ile Lys
 435 440 445

 Glu Gly Ser Met Ser Glu Asp Glu Phe Phe Gln Ala Gln Thr Met
 450 455 460

 Met Lys Leu Ser His Pro Lys Leu Val Lys Phe Tyr Gly Val Cys Ser
 465 470 475 480

 Lys Glu Tyr Pro Ile Tyr Ile Val Thr Glu Tyr Ile Ser Asn Gly Cys
 485 490 495

 Leu Leu Asn Tyr Leu Arg Ser His Gly Lys Gly Leu Glu Pro Ser Gln
 500 505 510

 Leu Leu Glu Met Cys Tyr Asp Val Cys Glu Gly Met Ala Phe Leu Glu
 515 520 525

 Ser His Gln Phe Ile His Arg Asp Leu Ala Ala Arg Asn Cys Leu Val
 530 535 540

 Asp Arg Asp Leu Cys Val Lys Val Ser Asp Phe Gly Met Thr Arg Tyr
 545 550 555 560

 Val Leu Asp Asp Gln Tyr Val Ser Ser Val Gly Thr Lys Phe Pro Val
 565 570 575

 Lys Trp Ser Ala Pro Glu Val Phe His Tyr Phe Lys Tyr Ser Ser Lys
 580 585 590

 Ser Asp Val Trp Ala Phe Gly Ile Leu Met Trp Glu Val Phe Ser Leu
 595 600 605

 Gly Lys Gln Pro Tyr Asp Leu Tyr Asp Asn Ser Gln Val Val Leu Lys
 610 615 620

 Val Ser Gln Gly His Arg Leu Tyr Arg Pro His Leu Ala Ser Asp Thr
 625 630 635 640

 Ile Tyr Gln Ile Met Tyr Ser Cys Trp His Glu Leu Pro Glu Lys Arg
 645 650 655

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 Asp Lys His
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agctcctgct cagtttgcc tcggggtagc acctccagcc acagaaaagca agccggtaag 180
tctctccagg taggacttgc tgcaacccag ctgctggact gatctgaaac gggactttgc 240
atactctccg aagtatggtg agttggtgct gacttcaaag ttgcctggtg aaggaagata 300
aggtgtggatcg cagagactaa ggggagaggg agaagccctg ctcctttct cccccaccaag 360
gcaca atg agc aac atc tgt cag agg ctc tgg gag tac cta gaa ccc tat 410
Met Ser Asn Ile Cys Gln Arg Leu Trp Glu Tyr Leu Glu Pro Tyr
1 5 10 15

ctc ccc tgt ttg tcc acg gag gca gac aag tca acc gtg att gaa aat 458
 Leu Pro Cys Leu Ser Thr Glu Ala Asp Lys Ser Thr Val Ile Glu Asn
 20 25 30

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gtg gct ttg ttt gat tac cag gct cgg act gct gag gac ttg agc ttc      554
Val Ala Leu Phe Asp Tyr Gln Ala Arg Thr Ala Glu Asp Leu Ser Phe
          50           55           60

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cga gca ggt gac aaa ctt caa gtt ctg gac act ttg cat gag ggc tgg      602
Arg Ala Gly Asp Lys Leu Gln Val Leu Asp Thr Leu His Glu Gly Trp
       65          70          75
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tgg ttt gcc aga cac ttg gag aaa aga cga gat ggc tcc agt cag caa 650
Trp Phe Ala Arg His Leu Glu Lys Arg Arg Asp Gly Ser Ser Gln Gln
80 85 90 95

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ctc caa ggc tat att cct tct aac tac gtg gct gag gac aga agc cta 698
Leu Gln Gly Tyr Ile Pro Ser Asn Tyr Val Ala Glu Asp Arg Ser Leu
100          105          110

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cag gca gag ccg tgg ttc ttt gga gca atc gga aga tca gat gca gag 746
Gln Ala Glu Pro Trp Phe Phe Gly Ala Ile Gly Arg Ser Asp Ala Glu
115 120 125

aaa caa cta tta tat tca gaa aac aag acc ggt tcc ttt cta atc aga		794	
Lys Gln Leu Leu Tyr Ser Glu Asn Lys Thr Gly Ser Phe Leu Ile Arg			
130	135	140	
gaa agt gaa agc caa aaa gga gaa ttc tct ctt tca gtt tta gat gga		842	
Glu Ser Glu Ser Gln Lys Gly Glu Phe Ser Leu Ser Val Leu Asp Gly			
145	150	155	
gca gtt gta aaa cac tac aga att aaa aga ctg gat gaa ggg gga ttt		890	
Ala Val Val Lys His Tyr Arg Ile Lys Arg Leu Asp Glu Gly Phe			
160	165	170	175
ttt ctc acg cga aga aga atc ttt tca aca ctg aac gaa ttt gtg agc		938	
Phe Leu Thr Arg Arg Ile Phe Ser Thr Leu Asn Glu Phe Val Ser			
180	185	190	
cac tac acc aag aca agt gac ggc ctg tgt gtc aag ctg ggg aaa cca		986	
His Tyr Thr Lys Thr Ser Asp Gly Leu Cys Val Lys Leu Gly Lys Pro			
195	200	205	
tgc tta aag atc cag gtc cca gct cca ttt gat ttg tcg tat aaa acc		1034	
Cys Leu Lys Ile Gln Val Pro Ala Pro Phe Asp Leu Ser Tyr Lys Thr			
210	215	220	
gtg gac caa tgg gag ata gac cgc aac tcc ata cag ctt ctg aag cga		1082	
Val Asp Gln Trp Glu Ile Asp Arg Asn Ser Ile Gln Leu Leu Lys Arg			
225	230	235	
ttg gga tct ggt cag ttt ggc gaa gta tgg gaa ggt ctg tgg aac aat		1130	
Leu Gly Ser Gly Gln Phe Gly Glu Val Trp Glu Gly Leu Trp Asn Asn			
240	245	250	255
acc act cca gta gca gtg aaa aca tta aaa cca ggt tca atg gat cca		1178	
Thr Thr Pro Val Ala Val Lys Thr Leu Lys Pro Gly Ser Met Asp Pro			
260	265	270	
aat gac ttc ctg agg gag gca cag ata atg aag aac cta aga cat cca		1226	
Asn Asp Phe Leu Arg Glu Ala Gln Ile Met Lys Asn Leu Arg His Pro			
275	280	285	
aag ctt atc cag ctt tat gct gtt tgc act tta gaa gat cca att tat		1274	
Lys Leu Ile Gln Leu Tyr Ala Val Cys Thr Leu Glu Asp Pro Ile Tyr			
290	295	300	
att att aca gag ttg atg aga cat gga agt ctg caa gaa tat ctc caa		1322	
Ile Ile Thr Glu Leu Met Arg His Gly Ser Leu Gln Glu Tyr Leu Gln			
305	310	315	
aat gac act gga tca aaa atc cat ctg act caa cag gta gac atg gcg		1370	
Asn Asp Thr Gly Ser Lys Ile His Leu Thr Gln Gln Val Asp Met Ala			
320	325	330	335
gca cag gtt gcc tct gga atg gcc tat ctg gag tct cggt aac tac att		1418	
Ala Gln Val Ala Ser Gly Met Ala Tyr Leu Glu Ser Arg Asn Tyr Ile			
340	345	350	

cac aga gat ctg gct gcc aga aat gtc ctc gtt ggt gaa cat aat atc His Arg Asp Leu Ala Ala Arg Asn Val Leu Val Gly Glu His Asn Ile 355 360 365	1466
tac aaa gta gca gat ttt gga ctt gcc aga gtt ttt aag gta gat aat Tyr Lys Val Ala Asp Phe Gly Leu Ala Arg Val Phe Lys Val Asp Asn 370 375 380	1514
gaa gac atc tat gaa tct aga cac gaa ata aag ctg ccg gtg aag tgg Glu Asp Ile Tyr Glu Ser Arg His Glu Ile Lys Leu Pro Val Lys Trp 385 390 395	1562
act gcg ccc gaa gcc att cgt agt aat aaa ttc agc att aag tcc gat Thr Ala Pro Glu Ala Ile Arg Ser Asn Lys Phe Ser Ile Lys Ser Asp 400 405 410 415	1610
gta tgg tca ttt gga atc ctt ctt tat gaa atc att act tat ggc aaa Val Trp Ser Phe Gly Ile Leu Leu Tyr Glu Ile Ile Thr Tyr Gly Lys 420 425 430	1658
atg cct tac agt ggt atg aca ggt gcc cag gta atc cag atg ttg gct Met Pro Tyr Ser Gly Met Thr Gly Ala Gln Val Ile Gln Met Leu Ala 435 440 445	1706
caa aac tat aga ctt ccg caa cca tcc aac tgt cca cag caa ttt tac Gln Asn Tyr Arg Leu Pro Gln Pro Ser Asn Cys Pro Gln Gln Phe Tyr 450 455 460	1754
aac atc atg ttg gag tgc tgg aat gca gag cct aag gaa cga cct aca Asn Ile Met Leu Glu Cys Trp Asn Ala Glu Pro Lys Glu Arg Pro Thr 465 470 475	1802
ttt gag aca ctg cgt tgg aaa ctt gaa gac tat ttt gaa aca gac tct Phe Glu Thr Leu Arg Trp Lys Leu Glu Asp Tyr Phe Glu Thr Asp Ser 480 485 490 495	1850
tca tat tca gat gca aat aac ttc ata aga tgaacactgg agaagaatat Ser Tyr Ser Asp Ala Asn Asn Phe Ile Arg 500 505	1900
caaataataa agtagcaaaa caaattcaaa taatccattc caaaatacaa tgtttatcaac 1960	
caactgcaca atcagtttat cctgacatat tcaagtgata ggataaagtt ggccatgtat 2020	
tatgaaaaag attatttgatg cattttatttgc actggggcaac actgcaggac agtcaaggc 2080	
atatataatt gctcaactgcc tggaaaatta agcacactaa accaagttat ttttcttttt 2140	
aagagatact tacatttcca tttattgttt gaaaatgtcgc gatcaagaga atcaacagat 2200	
gatagtccaa tttttactca gtgatgactg ttagcattt tcctgtttac tgatttagt 2260	
ggttattcat tattcctcag attgctgaat cccatcagggc tgttattatg aaggaattt 2320	
attgcttgc tgcacagcag gacctgtgct ttgagattt ttttctctt taaaaatatc 2380	
ctgtaactac aatgatggta aagccatgtt aaatgacttg attgtacttg gagtaattgc 2440	

acatTTTTT ctatgcataa aaaaatgatg cagctgttga gaaaacgaag tcttttcat 2500
 ttgcagaag gaaatgatgg aattttctg tacttcagta tgtgtcaact gagagtccata 2560
 tacatttagtt ttaatctctt aatattgaga atcagggttgc aaaacggatg agttattatc 2620
 tatggaaatg tgagaaatgt ctaatagccc ataaagtctg agaaataggt atcaaaatag 2680
 tttaggaaaa tgagaggaga acagtaggat tgctgtggcc tagacttctg agtaattaat 2740
 aaagaaaaaag aagtacccaa aaaaaaaaaa 2770

<210> 6
 <211> 505
 <212> PRT
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Megakaryocyte
 kinase 3

<400> 6
 Met Ser Asn Ile Cys Gln Arg Leu Trp Glu Tyr Leu Glu Pro Tyr Leu
 1 5 10 15
 Pro Cys Leu Ser Thr Glu Ala Asp Lys Ser Thr Val Ile Glu Asn Pro
 20 25 30
 Gly Ala Leu Cys Ser Pro Gln Ser Gln Arg His Gly His Tyr Phe Val
 35 40 45
 Ala Leu Phe Asp Tyr Gln Ala Arg Thr Ala Glu Asp Leu Ser Phe Arg
 50 55 60
 Ala Gly Asp Lys Leu Gln Val Leu Asp Thr Leu His Glu Gly Trp Trp
 65 70 75 80
 Phe Ala Arg His Leu Glu Lys Arg Arg Asp Gly Ser Ser Gln Gln Leu
 85 90 95
 Gln Gly Tyr Ile Pro Ser Asn Tyr Val Ala Glu Asp Arg Ser Leu Gln
 100 105 110
 Ala Glu Pro Trp Phe Phe Gly Ala Ile Gly Arg Ser Asp Ala Glu Lys
 115 120 125
 Gln Leu Leu Tyr Ser Glu Asn Lys Thr Gly Ser Phe Leu Ile Arg Glu
 130 135 140
 Ser Glu Ser Gln Lys Gly Glu Phe Ser Leu Ser Val Leu Asp Gly Ala
 145 150 155 160
 Val Val Lys His Tyr Arg Ile Lys Arg Leu Asp Glu Gly Gly Phe Phe
 165 170 175
 Leu Thr Arg Arg Arg Ile Phe Ser Thr Leu Asn Glu Phe Val Ser His
 180 185 190

Tyr Thr Lys Thr Ser Asp Gly Leu Cys Val Lys Leu Gly Lys Pro Cys
 195 200 205
 Leu Lys Ile Gln Val Pro Ala Pro Phe Asp Leu Ser Tyr Lys Thr Val
 210 215 220
 Asp Gln Trp Glu Ile Asp Arg Asn Ser Ile Gln Leu Leu Lys Arg Leu
 225 230 235 240
 Gly Ser Gly Gln Phe Gly Glu Val Trp Glu Gly Leu Trp Asn Asn Thr
 245 250 255
 Thr Pro Val Ala Val Lys Thr Leu Lys Pro Gly Ser Met Asp Pro Asn
 260 265 270
 Asp Phe Leu Arg Glu Ala Gln Ile Met Lys Asn Leu Arg His Pro Lys
 275 280 285
 Leu Ile Gln Leu Tyr Ala Val Cys Thr Leu Glu Asp Pro Ile Tyr Ile
 290 295 300
 Ile Thr Glu Leu Met Arg His Gly Ser Leu Gln Glu Tyr Leu Gln Asn
 305 310 315 320
 Asp Thr Gly Ser Lys Ile His Leu Thr Gln Gln Val Asp Met Ala Ala
 325 330 335
 Gln Val Ala Ser Gly Met Ala Tyr Leu Glu Ser Arg Asn Tyr Ile His
 340 345 350
 Arg Asp Leu Ala Ala Arg Asn Val Leu Val Gly Glu His Asn Ile Tyr
 355 360 365
 Lys Val Ala Asp Phe Gly Leu Ala Arg Val Phe Lys Val Asp Asn Glu
 370 375 380
 Asp Ile Tyr Glu Ser Arg His Glu Ile Lys Leu Pro Val Lys Trp Thr
 385 390 395 400
 Ala Pro Glu Ala Ile Arg Ser Asn Lys Phe Ser Ile Lys Ser Asp Val
 405 410 415
 Trp Ser Phe Gly Ile Leu Leu Tyr Glu Ile Ile Thr Tyr Gly Lys Met
 420 425 430
 Pro Tyr Ser Gly Met Thr Gly Ala Gln Val Ile Gln Met Leu Ala Gln
 435 440 445
 Asn Tyr Arg Leu Pro Gln Pro Ser Asn Cys Pro Gln Gln Phe Tyr Asn
 450 455 460
 Ile Met Leu Glu Cys Trp Asn Ala Glu Pro Lys Glu Arg Pro Thr Phe
 465 470 475 480
 Glu Thr Leu Arg Trp Lys Leu Glu Asp Tyr Phe Glu Thr Asp Ser Ser
 485 490 495

Tyr Ser Asp Ala Asn Asn Phe Ile Arg
500 505

<210> 7
<211> 450
<212> PRT
<213> *Homo sapiens*

<400> 7
Met Ser Ala Ile Gln Ala Ala Trp Pro Ser Gly Thr Glu Cys Ile Ala
1 5 10 15

Lys Tyr Asn Phe His Gly Thr Ala Glu Gln Asp Leu Pro Phe Cys Lys
 20 25 30

Gly Asp Val Leu Thr Ile Val Ala Val Thr Lys Asp Pro Asn Trp Tyr
35 40 45

Lys Ala Lys Asn Lys Val Gly Arg Glu Gly Ile Ile Pro Ala Asn Tyr
 50 55 60

Val Gln Lys Arg Glu Gly Val Lys Ala Gly Thr Lys Leu Ser Leu Met
65 70 75 800

Pro Trp Phe His Gly Lys Ile Thr Arg Glu Gln Ala Glu Arg Leu Leu
85 90 95

Tyr Pro Pro Glu Thr Gly Leu Phe Leu Val Arg Glu Ser Thr Asn Tyr
 100 105 110

Pro Gly Asp Tyr Thr Leu Cys Val Ser Cys Asp Gly Lys Val Glu His
 115 120 125

Tyr Arg Ile Met Tyr His Ala Ser Lys Leu Ser Ile Asp Glu Glu Val
130 135 140

Tyr Phe Glu Asn Leu Met Gln Leu Val Glu His Tyr Thr Ser Asp Ala
145 150 155 160

Asp Gly Leu Cys Thr Arg Leu Ile Lys Pro Lys Val Met Glu Gly Thr
165 .170 .175

Val Ala Ala Gln Asp Glu Phe Tyr Arg Ser Gly Trp Ala Leu Asn Met
180 185 190

Lys Glu Leu Lys Leu Leu Gln Thr Ile Gly Lys Gly Glu Phe Gly Asp
 195 200 205

Val Met Leu Gly Asp Tyr Arg Gly Asn Lys Val Ala Val Lys Cys Ile
210 215 220

Lys Asn Asp Ala Thr Ala Gln Ala Phe Leu Ala Glu Ala Ser Val Met
225 230 235 240

Ihr Gin Leu Arg His Ser Asn Leu Val Gin Leu Leu Gly Val Ile Val
245 250 255

Glu Glu Lys Gly Gly Leu Tyr Ile Val Thr Glu Tyr Met Ala Lys Gly
 260 265 270

Ser Leu Val Asp Tyr Leu Arg Ser Arg Gly Arg Ser Val Leu Gly Gly
 275 280 285

Asp Cys Leu Leu Lys Phe Ser Leu Asp Val Cys Glu Ala Met Glu Tyr
 290 295 300

Leu Glu Gly Asn Asn Phe Val His Arg Asp Leu Ala Ala Arg Asn Val
 305 310 315 320

Leu Val Ser Glu Asp Asn Val Ala Lys Val Ser Asp Phe Gly Leu Thr
 325 330 335

Lys Glu Ala Ser Ser Thr Gln Asp Thr Gly Lys Leu Pro Val Lys Trp
 340 345 350

Thr Ala Pro Glu Ala Leu Arg Glu Lys Lys Phe Ser Thr Lys Ser Asp
 355 360 365

Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile Tyr Ser Phe Gly Arg
 370 375 380

Val Pro Tyr Pro Arg Ile Pro Leu Lys Asp Val Val Pro Arg Val Glu
 385 390 395 400

Lys Gly Tyr Lys Met Asp Ala Pro Asp Gly Cys Pro Pro Ala Val Tyr
 405 410 415

Glu Val Met Lys Asn Cys Trp His Leu Asp Ala Ala Met Arg Pro Ser
 420 425 430

Phe Leu Gln Leu Arg Glu Gln Leu Glu His Ile Lys Thr His Glu Leu
 435 440 445

His Leu
 450

<210> 8
 <211> 659
 <212> PRT
 <213> Homo sapiens

<400> 8
 Met Ala Ala Val Ile Leu Glu Ser Ile Phe Leu Lys Arg Ser Gln Gln
 1 5 10 15

Lys Lys Lys Thr Ser Pro Leu Asn Phe Lys Lys Arg Leu Phe Leu Leu
 20 25 30

Thr Val His Lys Leu Ser Tyr Tyr Glu Tyr Asp Phe Glu Arg Gly Arg
 35 40 45

Arg Gly Ser Lys Lys Gly Ser Ile Asp Val Glu Lys Ile Thr Cys Val
 50 55 60

Glu Thr Val Val Pro Glu Lys Asn Pro Pro Pro Glu Arg Gln Ile Pro
 65 70 75 80

Arg Arg Gly Glu Glu Ser Ser Glu Met Glu Gln Ile Ser Ile Ile Glu
 85 90 95

Arg Phe Pro Tyr Pro Phe Gln Val Val Tyr Asp Glu Gly Pro Leu Tyr
 100 105 110

Val Phe Ser Pro Thr Glu Glu Leu Arg Lys Arg Trp Ile His Gln Leu
 115 120 125

Lys Asn Val Ile Arg Tyr Asn Ser Asp Leu Val Gln Lys Tyr His Pro
 130 135 140

Cys Phe Trp Ile Asp Gly Gln Tyr Leu Cys Cys Ser Gln Thr Ala Lys
 145 150 155 160

Asn Ala Met Gly Cys Gln Ile Leu Glu Asn Arg Asn Gly Ser Leu Lys
 165 170 175

Pro Gly Ser Ser His Arg Lys Thr Lys Lys Pro Leu Pro Pro Thr Pro
 180 185 190

Glu Glu Asp Gln Ile Leu Lys Lys Pro Leu Pro Pro Glu Pro Ala Ala
 195 200 205

Ala Pro Val Ser Thr Ser Glu Leu Lys Lys Val Val Ala Leu Tyr Asp
 210 215 220

Tyr Met Pro Met Asn Ala Asn Asp Leu Gln Leu Arg Lys Gly Asp Glu
 225 230 235 240

Tyr Phe Ile Leu Glu Glu Ser Asn Leu Pro Trp Trp Arg Ala Arg Asp
 245 250 255

Lys Asn Gly Gln Glu Gly Tyr Ile Pro Ser Asn Tyr Val Thr Glu Ala
 260 265 270

Glu Asp Ser Ile Glu Met Tyr Glu Trp Tyr Ser Lys His Met Thr Arg
 275 280 285

Ser Gln Ala Glu Gln Leu Leu Lys Gln Glu Gly Lys Glu Gly Gly Phe
 290 295 300

Ile Val Arg Asp Ser Ser Lys Ala Gly Lys Tyr Thr Val Ser Val Phe
 305 310 315 320

Ala Lys Ser Thr Gly Asp Pro Gln Gly Val Ile Arg His Tyr Val Val
 325 330 335

Cys Ser Thr Pro Gln Ser Gln Tyr Tyr Leu Ala Glu Lys His Leu Phe
 340 345 350

Ser Thr Ile Pro Glu Leu Ile Asn Tyr His Gln His Asn Ser Ala Gly
 355 360 365

Leu Ile Ser Arg Leu Lys Tyr Pro Val Ser Gln Gln Asn Lys Asn Ala
 370 375 380

 Pro Ser Thr Ala Gly Leu Gly Tyr Gly Ser Trp Glu Ile Asp Pro Lys
 385 390 395 400

 Asp Leu Thr Phe Leu Lys Glu Leu Gly Thr Gly Gln Phe Gly Val Val
 405 410 415

 Lys Tyr Gly Lys Trp Arg Gly Gln Tyr Asp Val Ala Ile Lys Met Ile
 420 425 430

 Lys Glu Gly Ser Met Ser Glu Asp Glu Phe Ile Glu Glu Ala Lys Val
 435 440 445

 Met Met Asn Leu Ser His Glu Lys Leu Val Gln Leu Tyr Gly Val Cys
 450 455 460

 Thr Lys Gln Arg Pro Ile Phe Ile Ile Thr Glu Tyr Met Ala Asn Gly
 465 470 475 480

 Cys Leu Leu Asn Tyr Leu Arg Glu Met Arg His Arg Phe Gln Thr Gln
 485 490 495

 Gln Leu Leu Glu Met Cys Lys Asp Val Cys Glu Ala Met Glu Tyr Leu
 500 505 510

 Glu Ser Lys Gln Phe Leu His Arg Asp Leu Ala Ala Arg Asn Cys Leu
 515 520 525

 Val Asn Asp Gln Gly Val Val Lys Val Ser Asp Phe Gly Leu Ser Arg
 530 535 540

 Tyr Val Leu Asp Asp Glu Tyr Thr Ser Ser Val Gly Ser Lys Phe Pro
 545 550 555 560

 Val Arg Trp Ser Pro Pro Glu Val Leu Met Tyr Ser Lys Phe Ser Ser
 565 570 575

 Lys Ser Asp Ile Trp Ala Phe Gly Val Leu Met Trp Glu Ile Tyr Ser
 580 585 590

 Leu Gly Lys Met Pro Tyr Glu Arg Phe Thr Asn Ser Glu Thr Ala Glu
 595 600 605

 His Ile Ala Gln Gly Leu Arg Leu Tyr Arg Pro His Leu Ala Ser Glu
 610 615 620

 Lys Val Tyr Thr Ile Met Tyr Ser Cys Trp His Glu Lys Ala Asp Glu
 625 630 635 640

 Arg Pro Thr Phe Lys Ile Leu Leu Ser Asn Ile Leu Asp Val Met Asp
 645 650 655

 Glu Glu Ser

<210> 9
<211> 620
<212> PRT
<213> Homo sapiens

<400> 9
Met Asn Asn Phe Ile Leu Leu Glu Glu Gln Leu Ile Lys Lys Ser Gln
1 5 10 15
Gln Lys Arg Arg Thr Ser Pro Ser Asn Phe Lys Val Arg Phe Phe Val
20 25 30
Leu Thr Lys Ala Ser Leu Ala Tyr Phe Glu Asp Arg His Gly Lys Lys
35 40 45
Arg Thr Leu Lys Gly Ser Ile Glu Leu Ser Arg Ile Lys Cys Val Glu
50 55 60
Ile Val Lys Ser Asp Ile Ser Ile Pro Cys His Tyr Lys Tyr Pro Phe
65 70 75 80
Gln Val Val His Asp Asn Tyr Leu Leu Tyr Val Phe Ala Pro Asp Arg
85 90 95
Glu Ser Arg Gln Arg Trp Val Leu Ala Leu Lys Glu Glu Thr Arg Asn
100 105 110
Asn Asn Ser Leu Val Pro Lys Tyr His Pro Asn Phe Trp Met Asp Gly
115 120 125
Lys Trp Arg Cys Cys Ser Gln Leu Glu Lys Leu Ala Thr Gly Cys Ala
130 135 140
Gln Tyr Asp Pro Thr Lys Asn Ala Ser Lys Lys Pro Leu Pro Pro Thr
145 150 155 160
Pro Glu Asp Asn Arg Arg Pro Leu Trp Glu Pro Glu Glu Thr Val Val
165 170 175
Ile Ala Leu Tyr Asp Tyr Gln Thr Asn Asp Pro Gln Glu Leu Ala Leu
180 185 190
Arg Arg Asn Glu Glu Tyr Cys Leu Leu Asp Ser Ser Glu Ile His Trp
195 200 205
Trp Arg Val Gln Asp Arg Asn Gly His Glu Gly Tyr Val Pro Ser Ser
210 215 220
Tyr Leu Val Glu Lys Ser Pro Asn Asn Leu Glu Thr Tyr Glu Trp Tyr
225 230 235 240
Asn Lys Ser Ile Ser Arg Asp Lys Ala Glu Lys Leu Leu Leu Asp Thr
245 250 255
Gly Lys Glu Gly Ala Phe Met Val Arg Asp Ser Arg Thr Ala Gly Thr
260 265 270

Tyr Thr Val Ser Val Phe Thr Lys Ala Val Val Ser Glu Asn Asn Pro
 275 280 285

Cys Ile Lys His Tyr His Ile Lys Glu Thr Asn Asp Asn Pro Lys Arg
 290 295 300

Tyr Tyr Val Ala Glu Lys Tyr Val Phe Asp Ser Ile Pro Leu Leu Ile
 305 310 315 320

Asn Tyr His Gln His Asn Gly Gly Leu Val Thr Arg Leu Arg Tyr
 325 330 335

Pro Val Cys Phe Gly Arg Gln Lys Ala Pro Val Thr Ala Gly Leu Arg
 340 345 350

Tyr Gly Lys Trp Val Ile Asp Pro Ser Glu Leu Thr Phe Val Gln Glu
 355 360 365

Ile Gly Ser Gly Gln Phe Gly Leu Val His Leu Gly Tyr Trp Leu Asn
 370 375 380

Lys Asp Lys Val Ala Ile Lys Thr Ile Arg Glu Gly Ala Met Ser Glu
 385 390 395 400

Glu Asp Phe Ile Glu Glu Ala Glu Val Met Met Lys Leu Ser His Pro
 405 410 415

Lys Leu Val Gln Leu Tyr Gly Val Cys Leu Glu Gln Ala Pro Ile Cys
 420 425 430

Leu Val Phe Glu Phe Met Glu His Gly Cys Leu Ser Asp Tyr Leu Arg
 435 440 445

Thr Gln Arg Gly Leu Phe Ala Ala Glu Thr Leu Leu Gly Met Cys Leu
 450 455 460

Asp Val Cys Glu Gly Met Ala Tyr Leu Glu Glu Ala Cys Val Ile His
 465 470 475 480

Arg Asp Leu Ala Ala Arg Asn Cys Leu Val Gly Glu Asn Gln Val Ile
 485 490 495

Lys Val Ser Asp Phe Gly Met Thr Arg Phe Val Leu Asp Asp Gln Tyr
 500 505 510

Thr Ser Ser Thr Gly Thr Lys Phe Pro Val Lys Trp Ala Ser Pro Glu
 515 520 525

Val Phe Ser Phe Ser Arg Tyr Ser Ser Lys Ser Asp Val Trp Ser Phe
 530 535 540

Gly Val Leu Met Trp Glu Val Phe Ser Glu Gly Lys Ile Pro Tyr Glu
 545 550 555 560

Asn Arg Ser Asn Ser Glu Val Val Glu Asp Ile Ser Thr Gly Phe Arg
 565 570 575

Leu Tyr Lys Pro Arg Leu Ala Ser Thr His Val Tyr Gln Ile Met Asn
580 585 590

His Cys Trp Lys Glu Arg Pro Glu Asp Arg Pro Ala Phe Ser Arg Leu
595 600 605

Leu Arg Gln Leu Ala Glu Ile Ala Glu Ser Gly Leu
610 615 620

<210> 10
<211> 527
<212> PRT
<213> Mus sp.

<400> 10
Met Met Val Ser Phe Pro Val Lys Ile Asn Phe His Ser Ser Pro Gln
1 5 10 15

Ser Arg Asp Arg Trp Val Lys Lys Leu Lys Glu Glu Ile Lys Asn Asn
20 25 30

Asn Asn Ile Met Ile Lys Tyr His Pro Lys Phe Trp Ala Asp Gly Ser
 35 40 45

Tyr Gln Cys Cys Arg Gln Thr Glu Lys Leu Ala Pro Gly Cys Glu Lys
 50 55 60

Tyr Asn Leu Phe Glu Ser Ser Ile Arg Lys Thr Leu Pro Pro Ala Pro
65 70 75 80

Glu Ile Lys Lys Arg Arg Pro Pro Pro Pro Ile Pro Pro Glu Glu Glu
85 90 95

Asn	Thr	Glu	Glu	Ile	Val	Val	Ala	Met	Tyr	Asp	Phe	Gln	Ala	Thr	Glu
		100						105					110		

Ala His Asp Leu Arg Leu Glu Arg Gly Gln Glu Tyr Ile Ile Leu Glu
115 120 125

Lys Asn Asp Leu His Trp Trp Arg Ala Arg Asp Lys Tyr Gly Trp Tyr
130 135 140

Cys Arg Asn Thr Asn Arg Ser Lys Ala Glu Gln Leu Leu Arg Thr Glu
 145 150 155 160

Asp Lys Glu Gly Gly Phe Met Val Arg Asp Ser Ser Gln Pro Gly Leu
165 170 175

Tyr Thr Val Ser Leu Tyr Thr Lys Phe Gly Gly Glu Gly Ser Ser Gly
 180 185 190

Phe Arg His Tyr His Ile Lys Glu Thr Ala Thr Ser Pro Lys Lys Tyr
195 200 205

Tyr Leu Ala Glu Lys His Ala Phe Gly Ser Ile Pro Glu Ile Ile Glu
210 215 220

Tyr His Lys His Asn Ala Ala Gly Leu Val Thr Arg Leu Arg Tyr Pro
 225 230 235 240

Val Ser Thr Lys Gly Lys Asn Ala Pro Thr Thr Ala Gly Phe Ser Tyr
 245 250 255

Asp Lys Trp Glu Ile Asn Pro Ser Glu Leu Thr Phe Met Arg Glu Leu
 260 265 270

Gly Ser Gly Leu Phe Gly Val Val Arg Leu Gly Lys Trp Arg Ala Gln
 275 280 285

Tyr Lys Val Ala Ile Lys Ala Ile Arg Glu Gly Ala Met Cys Glu Glu
 290 295 300

Asp Phe Ile Glu Glu Ala Lys Val Met Met Lys Leu Thr His Pro Lys
 305 310 315 320

Leu Val Gln Leu Tyr Gly Val Cys Thr Gln Gln Lys Pro Ile Tyr Ile
 325 330 335

Val Thr Glu Phe Met Glu Arg Gly Cys Leu Leu Asn Phe Leu Arg Gln
 340 345 350

Arg Gln Gly His Phe Ser Arg Asp Met Leu Leu Ser Met Cys Gln Asp
 355 360 365

Val Cys Glu Gly Met Glu Tyr Leu Glu Arg Asn Ser Phe Ile His Arg
 370 375 380

Asp Leu Ala Ala Arg Asn Cys Leu Val Asn Glu Ala Gly Val Val Lys
 385 390 395 400

Val Ser Asp Phe Gly Met Ala Arg Tyr Val Leu Asp Asp Gln Tyr Thr
 405 410 415

Ser Ser Ser Gly Ala Lys Phe Pro Val Lys Trp Cys Pro Pro Glu Val
 420 425 430

Phe Asn Tyr Ser Arg Phe Ser Ser Lys Ser Asp Val Trp Ser Phe Gly
 435 440 445

Val Leu Met Trp Glu Ile Phe Thr Glu Gly Arg Met Pro Phe Glu Lys
 450 455 460

Asn Thr Asn Tyr Glu Val Val Thr Met Val Thr Arg Gly His Arg Leu
 465 470 475 480

His Arg Pro Lys Leu Ala Thr Lys Tyr Leu Tyr Glu Val Met Leu Arg
 485 490 495

Cys Trp Gln Glu Arg Pro Glu Gly Arg Pro Ser Phe Glu Asp Leu Leu
 500 505 510

Arg Thr Ile Asp Glu Leu Val Glu Cys Glu Glu Thr Phe Gly Arg
 515 520 525

<210> 11
<211> 537
<212> PRT
<213> Homo sapiens

<400> 11
Met Gly Cys Val Gln Cys Lys Asp Lys Glu Ala Thr Lys Leu Thr Glu
1 5 10 15
Glu Arg Asp Gly Ser Leu Asn Gln Ser Ser Gly Tyr Arg Tyr Gly Thr
20 25 30
Asp Pro Thr Pro Gln His Tyr Pro Ser Phe Gly Val Thr Ser Ile Pro
35 40 45
Asn Tyr Asn Asn Phe His Ala Ala Gly Gly Gln Gly Leu Thr Val Phe
50 55 60
Gly Gly Val Asn Ser Ser His Thr Gly Thr Leu Arg Thr Arg Gly
65 70 75 80
Gly Thr Gly Val Thr Leu Phe Val Ala Leu Tyr Asp Tyr Glu Ala Arg
85 90 95
Thr Glu Asp Asp Leu Ser Phe His Lys Gly Glu Lys Phe Gln Ile Leu
100 105 110
Asn Ser Ser Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Thr Thr Gly
115 120 125
Glu Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile
130 135 140
Gln Ala Glu Glu Trp Tyr Phe Gly Lys Leu Gly Arg Lys Asp Ala Glu
145 150 155 160
Arg Gln Leu Leu Ser Phe Gly Asn Pro Arg Gly Thr Phe Leu Ile Arg
165 170 175
Glu Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp
180 185 190
Asp Asp Met Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu
195 200 205
Asp Asn Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Glu Thr Leu
210 215 220
Gln Gln Leu Val Gln His Tyr Ser Glu Arg Ala Ala Gly Leu Cys Cys
225 230 235 240
Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu
245 250 255
Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln
260 265 270

Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly
 275 280 285

Thr Trp Asn Gly Asn Thr Lys Val Ala Ile Lys Thr Leu Lys Pro Gly
 290 295 300

Thr Met Ser Pro Glu Ser Phe Leu Glu Glu Ala Gln Ile Met Lys Lys
 305 310 315 320

Leu Lys His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu
 325 330 335

Pro Ile Tyr Ile Val Thr Glu Tyr Met Asn Lys Gly Ser Leu Leu Asp
 340 345 350

Phe Leu Lys Asp Gly Glu Gly Arg Ala Leu Lys Leu Pro Asn Leu Val
 355 360 365

Asp Met Ala Ala Gln Val Ala Ala Gly Met Ala Tyr Ile Glu Arg Met
 370 375 380

Asn Tyr Ile His Arg Asp Leu Arg Ser Ala Asn Ile Leu Val Gly Asn
 385 390 395 400

Gly Leu Ile Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu
 405 410 415

Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp
 420 425 430

Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp
 435 440 445

Val Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg
 450 455 460

Val Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu
 465 470 475 480

Arg Gly Tyr Arg Met Pro Cys Pro Gln Asp Cys Pro Ile Ser Leu His
 485 490 495

Glu Leu Met Ile His Cys Trp Lys Lys Asp Pro Glu Glu Arg Pro Thr
 500 505 510

Phe Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu
 515 520 525

Pro Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535

<210> 12
<211> 536
<212> PRT
<213> Gallus gallus

<400> 12
 Met Gly Cys Val His Cys Lys Glu Lys Ile Ser Gly Lys Gly Gln Gly
 1 5 10 15
 Gly Ser Gly Thr Gly Thr Pro Ala His Pro Pro Ser Gln Tyr Asp Pro
 20 25 30
 Asp Pro Thr Gln Leu Ser Gly Ala Phe Thr His Ile Pro Asp Phe Asn
 35 40 45
 Asn Phe His Ala Ala Ala Val Ser Pro Pro Val Pro Phe Ser Gly Pro
 50 55 60
 Gly Phe Tyr Pro Cys Asn Thr Leu Gln Ala His Ser Ser Ile Thr Gly
 65 70 75 80
 Gly Gly Val Thr Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr
 85 90 95
 Glu Asp Asp Leu Ser Phe Gln Lys Gly Glu Lys Phe His Ile Ile Asn
 100 105 110
 Asn Thr Glu Gly Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Ala
 115 120 125
 Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln
 130 135 140
 Ala Glu Glu Trp Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg
 145 150 155 160
 Gln Leu Leu Cys His Gly Asn Cys Arg Gly Thr Phe Leu Ile Arg Glu
 165 170 175
 Ser Glu Thr Thr Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp
 180 185 190
 Glu Ala Lys Gly Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp
 195 200 205
 Ser Gly Gly Tyr Tyr Ile Thr Thr Arg Ala Gln Phe Asp Thr Ile Gln
 210 215 220
 Gln Leu Val Gln His Tyr Ile Glu Arg Ala Ala Gly Leu Cys Cys Arg
 225 230 235 240
 Leu Ala Val Pro Cys Pro Lys Gly Thr Pro Lys Leu Ala Asp Leu Ser
 245 250 255
 Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln Leu
 260 265 270
 Leu Gln Lys Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly Thr
 275 280 285
 Trp Asn Gly Thr Thr Lys Val Ala Val Lys Thr Leu Lys Pro Gly Thr
 290 295 300

Met Ser Pro Glu Ala Phe Leu Glu Glu Ala Gln Ile Met Lys Arg Leu
 305 310 315 320

Arg His Asp Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335

Ile Tyr Ile Val Thr Glu Phe Met Ser Gln Gly Ser Leu Leu Asp Phe
 340 345 350

Leu Lys Asp Gly Asp Gly Arg Tyr Leu Lys Leu Pro Gln Leu Val Asp
 355 360 365

Met Ala Ala Gln Ile Ala Ala Gly Met Ala Tyr Ile Glu Arg Met Asn
 370 375 380

Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Asp Asn
 385 390 395 400

Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
 420 425 430

Ala Pro Glu Ala Ala Leu Phe Gly Lys Phe Thr Ile Lys Ser Asp Val
 435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Val Thr Lys Gly Arg Val
 450 455 460

Pro Tyr Pro Gly Met Asn Asn Arg Glu Val Leu Glu Gln Val Glu Arg
 465 470 475 480

Gly Tyr Arg Met Gln Cys Pro Gly Gly Cys Pro Pro Ser Leu His Asp
 485 490 495

Val Met Val Gln Cys Trp Lys Arg Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510

Glu Tyr Leu Gln Ser Phe Leu Glu Asp Tyr Phe Thr Ala Thr Glu Pro
 515 520 525

Gln Tyr Gln Pro Gly Asp Asn Gln
 530 535

<210> 13
 <211> 536
 <212> PRT
 <213> Homo sapiens

<400> 13
 Met Gly Ser Asn Lys Ser Lys Pro Lys Asp Ala Ser Gln Arg Arg Arg
 1 5 10 15

Ser Leu Glu Pro Ala Glu Asn Val His Gly Ala Gly Gly Ala Phe
 20 25 30

Pro Ala Ser Gln Thr Pro Ser Lys Pro Ala Ser Ala Asp Gly His Arg
 35 40 45
 Gly Pro Ser Ala Ala Phe Ala Pro Ala Ala Ala Glu Pro Lys Leu Phe
 50 55 60
 Gly Gly Phe Asn Ser Ser Asp Thr Val Thr Ser Pro Gln Arg Ala Gly
 65 70 75 80
 Pro Leu Ala Gly Gly Val Thr Thr Phe Val Ala Leu Tyr Asp Tyr Glu
 85 90 95
 Ser Arg Thr Glu Thr Asp Leu Ser Phe Lys Lys Gly Glu Arg Leu Gln
 100 105 110
 Ile Val Asn Asn Thr Glu Gly Asp Trp Trp Leu Ala His Ser Leu Ser
 115 120 125
 Thr Gly Gln Thr Gly Tyr Ile Pro Ser Asn Tyr Val Ala Pro Ser Asp
 130 135 140
 Ser Ile Gln Ala Glu Glu Trp Tyr Phe Gly Lys Ile Thr Arg Arg Glu
 145 150 155 160
 Ser Glu Arg Leu Leu Leu Asn Ala Glu Asn Pro Arg Gly Thr Phe Leu
 165 170 175
 Val Arg Glu Ser Glu Thr Thr Lys Gly Ala Tyr Cys Leu Ser Val Ser
 180 185 190
 Asp Phe Asp Asn Ala Lys Gly Leu Asn Val Lys His Tyr Lys Ile Arg
 195 200 205
 Lys Leu Asp Ser Gly Gly Phe Tyr Ile Thr Ser Arg Thr Gln Phe Asn
 210 215 220
 Ser Leu Gln Gln Leu Val Ala Tyr Tyr Ser Lys His Ala Asp Gly Leu
 225 230 235 240
 Cys His Arg Leu Thr Thr Val Cys Pro Thr Ser Lys Pro Gln Thr Gln
 245 250 255
 Gly Leu Ala Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser Leu Arg Leu
 260 265 270
 Glu Val Lys Leu Gly Gln Gly Cys Phe Gly Glu Val Trp Met Gly Thr
 275 280 285
 Trp Asn Gly Thr Thr Arg Val Ala Ile Lys Thr Leu Lys Pro Gly Thr
 290 295 300
 Met Ser Pro Glu Ala Phe Leu Gln Glu Ala Gln Val Met Lys Lys Leu
 305 310 315 320
 Arg His Glu Lys Leu Val Gln Leu Tyr Ala Val Val Ser Glu Glu Pro
 325 330 335

Ile Tyr Ile Val Thr Glu Tyr Met Ser Lys Gly Ser Leu Leu Asp Phe
 340 345 350

Leu Lys Gly Glu Thr Gly Lys Tyr Leu Arg Leu Pro Gln Leu Val Asp
 355 360 365

Met Ala Ala Gln Ile Ala Ser Gly Met Ala Tyr Val Glu Arg Met Asn
 370 375 380

Tyr Val His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Gly Glu Asn
 385 390 395 400

Leu Val Cys Lys Val Ala Asp Phe Gly Leu Ala Arg Leu Ile Glu Asp
 405 410 415

Asn Glu Tyr Thr Ala Arg Gln Gly Ala Lys Phe Pro Ile Lys Trp Thr
 420 425 430

Ala Pro Glu Ala Ala Leu Tyr Gly Arg Phe Thr Ile Lys Ser Asp Val
 435 440 445

Trp Ser Phe Gly Ile Leu Leu Thr Glu Leu Thr Thr Lys Gly Arg Val
 450 455 460

Pro Tyr Pro Gly Met Val Asn Arg Glu Val Leu Asp Gln Val Glu Arg
 465 470 475 480

Gly Tyr Arg Met Pro Cys Pro Pro Glu Cys Pro Glu Ser Leu His Asp
 485 490 495

Leu Met Cys Gln Cys Trp Arg Lys Glu Pro Glu Glu Arg Pro Thr Phe
 500 505 510

Glu Tyr Leu Gln Ala Phe Leu Glu Asp Tyr Phe Thr Ser Thr Glu Pro
 515 520 525

Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535

<210> 14
<211> 543
<212> PRT
<213> Homo sapiens

<400> 14
Met Gly Cys Ile Lys Ser Lys Glu Asn Lys Ser Pro Ala Ile Lys Tyr
 1 5 10 15

Arg Pro Glu Asn Thr Pro Glu Pro Val Ser Thr Ser Val Ser His Tyr
 20 25 30

Gly Ala Glu Pro Thr Thr Val Ser Pro Cys Pro Ser Ser Ser Ala Lys
 35 40 45

Gly Thr Ala Val Asn Phe Ser Ser Leu Ser Met Thr Pro Phe Gly Gly
 50 55 60

Ser Ser Gly Val Thr Pro Phe Gly Gly Ala Ser Ser Ser Phe Ser Val
 65 70 75 80

Val Pro Ser Ser Tyr Pro Ala Gly Leu Thr Gly Gly Val Thr Ile Phe
 85 90 95

Val Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Thr Glu Asp Leu Ser Phe
 100 105 110

Lys Lys Gly Glu Arg Phe Gln Ile Ile Asn Asn Thr Glu Gly Asp Trp
 115 120 125

Trp Glu Ala Arg Ser Ile Ala Thr Gly Lys Asn Gly Tyr Ile Pro Ser
 130 135 140

Asn Tyr Val Ala Pro Ala Asp Ser Ile Gln Ala Glu Glu Trp Tyr Phe
 145 150 155 160

Gly Lys Met Gly Arg Lys Asp Ala Glu Arg Leu Leu Leu Asn Pro Gly
 165 170 175

Asn Gln Arg Gly Ile Phe Leu Val Arg Glu Ser Glu Thr Thr Lys Gly
 180 185 190

Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Glu Ile Arg Gly Asp Asn
 195 200 205

Val Lys His Tyr Lys Ile Arg Lys Leu Asp Asn Gly Gly Tyr Tyr Ile
 210 215 220

Thr Thr Arg Ala Gln Phe Asp Thr Leu Gln Lys Leu Val Lys His Tyr
 225 230 235 240

Thr Glu His Ala Asp Gly Leu Cys His Lys Leu Thr Thr Val Cys Pro
 245 250 255

Thr Val Lys Pro Gln Thr Gln Gly Leu Ala Lys Asp Ala Trp Glu Ile
 260 265 270

Pro Arg Glu Ser Leu Arg Leu Glu Val Lys Leu Gly Gln Gly Cys Phe
 275 280 285

Gly Glu Val Trp Met Gly Thr Trp Asn Gly Thr Thr Lys Val Ala Ile
 290 295 300

Lys Thr Leu Lys Pro Gly Thr Met Met Pro Glu Ala Phe Leu Gln Glu
 305 310 315 320

Ala Gln Ile Met Lys Lys Leu Arg His Asp Lys Leu Val Pro Leu Tyr
 325 330 335

Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe Met Ser
 340 345 350

Lys Gly Ser Leu Leu Asp Phe Leu Lys Glu Gly Asp Gly Lys Tyr Leu
 355 360 365

Lys Leu Pro Gln Leu Val Asp Met Ala Ala Gln Ile Ala Asp Gly Met
 370 375 380
 Ala Tyr Ile Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 385 390 395 400
 Asn Ile Leu Val Gly Glu Asn Leu Val Cys Lys Ile Ala Asp Phe Gly
 405 410 415
 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Gln Gly Ala
 420 425 430
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Tyr Gly Arg
 435 440 445
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Gln Thr Glu
 450 455 460
 Leu Val Thr Lys Gly Arg Val Pro Tyr Pro Gly Met Val Asn Arg Glu
 465 470 475 480
 Val Leu Glu Gln Val Glu Arg Gly Tyr Arg Met Pro Cys Pro Gln Gly
 485 490 495
 Cys Pro Glu Ser Leu His Glu Leu Met Asn Leu Cys Trp Lys Lys Asp
 500 505 510
 Pro Asp Glu Arg Pro Thr Phe Glu Tyr Ile Gln Ser Phe Leu Glu Asp
 515 520 525
 Tyr Phe Thr Ala Thr Glu Pro Gln Tyr Gln Pro Gly Glu Asn Leu
 530 535 540

<210> 15
 <211> 529
 <212> PRT
 <213> Homo sapiens

<400> 15
 Met Gly Cys Val Phe Cys Lys Lys Leu Glu Pro Val Ala Thr Ala Lys
 1 5 10 15
 Glu Asp Ala Gly Leu Glu Gly Asp Phe Arg Ser Tyr Gly Ala Ala Asp
 20 25 30
 His Tyr Gly Pro Asp Pro Thr Lys Ala Arg Pro Ala Ser Ser Phe Ala
 35 40 45
 His Ile Pro Asn Tyr Ser Asn Phe Ser Ser Gln Ala Ile Asn Pro Gly
 50 55 60
 Phe Leu Asp Ser Gly Thr Ile Arg Gly Val Ser Gly Ile Gly Val Thr
 65 70 75 80
 Leu Phe Ile Ala Leu Tyr Asp Tyr Glu Ala Arg Thr Glu Asp Asp Leu
 85 90 95

Thr Phe Thr Lys Gly Glu Lys Phe His Ile Leu Asn Asn Thr Glu Gly
 100 105 110

Asp Trp Trp Glu Ala Arg Ser Leu Ser Ser Gly Lys Thr Gly Cys Ile
 115 120 125

Pro Ser Asn Tyr Val Ala Pro Val Asp Ser Ile Gln Ala Glu Glu Trp
 130 135 140

Tyr Phe Gly Lys Ile Gly Arg Lys Asp Ala Glu Arg Gln Leu Leu Ser
 145 150 155 160

Pro Gly Asn Pro Gln Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr Thr
 165 170 175

Lys Gly Ala Tyr Ser Leu Ser Ile Arg Asp Trp Asp Gln Thr Arg Gly
 180 185 190

Asp His Val Lys His Tyr Lys Ile Arg Lys Leu Asp Met Gly Gly Tyr
 195 200 205

Tyr Ile Thr Thr Arg Val Gln Phe Asn Ser Val Gln Glu Leu Val Gln
 210 215 220

His Tyr Met Glu Val Asn Asp Gly Leu Cys Asn Leu Leu Ile Ala Pro
 225 230 235 240

Cys Thr Ile Met Lys Pro Gln Thr Leu Gly Leu Ala Lys Asp Ala Trp
 245 250 255

Glu Ile Ser Arg Ser Ser Ile Thr Leu Glu Arg Arg Leu Gly Thr Gly
 260 265 270

Cys Phe Gly Asp Val Trp Leu Gly Thr Trp Asn Gly Ser Thr Lys Val
 275 280 285

Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Pro Lys Ala Phe Leu
 290 295 300

Glu Glu Ala Gln Val Met Lys Leu Leu Arg His Asp Lys Leu Val Gln
 305 310 315 320

Leu Tyr Ala Val Val Ser Glu Glu Pro Ile Tyr Ile Val Thr Glu Phe
 325 330 335

Met Cys His Gly Ser Leu Leu Asp Phe Leu Lys Asn Pro Glu Gly Gln
 340 345 350

Asp Leu Arg Leu Pro Gln Leu Val Asp Met Ala Ala Gln Val Ala Glu
 355 360 365

Gly Met Ala Tyr Met Glu Arg Met Asn Tyr Ile His Arg Asp Leu Arg
 370 375 380

Ala Ala Asn Ile Leu Val Gly Glu Arg Leu Ala Cys Lys Ile Ala Asp
 385 390 395 400

Phe Gly Leu Ala Arg Leu Ile Lys Asp Asp Glu Tyr Asn Pro Cys Gln
 405 410 415

Gly Ser Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ala Leu Phe
 420 425 430

Gly Arg Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu
 435 440 445

Thr Glu Leu Ile Thr Lys Gly Arg Ile Pro Tyr Pro Gly Met Asn Lys
 450 455 460

Arg Glu Val Leu Glu Gln Val Glu Gln Gly Tyr His Met Pro Cys Pro
 465 470 475 480

Pro Gly Cys Pro Ala Ser Leu Tyr Glu Ala Met Glu Gln Thr Trp Arg
 485 490 495

Leu Asp Pro Glu Glu Arg Pro Thr Phe Glu Tyr Leu Gln Ser Phe Leu
 500 505 510

Glu Asp Tyr Phe Thr Ser Ala Glu Pro Gln Tyr Gln Pro Gly Asp Gln
 515 520 525

Thr

<210> 16
<211> 512
<212> PRT
<213> Homo sapiens

<400> 16
Met Gly Cys Ile Lys Ser Lys Gly Lys Asp Ser Leu Ser Asp Asp Gly
 1 5 10 15

Val Asp Leu Lys Thr Gln Pro Val Arg Asn Thr Glu Arg Thr Ile Tyr
 20 25 30

Val Arg Asp Pro Thr Ser Asn Lys Gln Gln Arg Pro Val Pro Glu Ser
 35 40 45

Gln Leu Leu Pro Gly Gln Arg Phe Gln Thr Lys Asp Pro Glu Glu Gln
 50 55 60

Gly Asp Ile Val Val Ala Leu Tyr Pro Tyr Asp Gly Ile His Pro Asp
 65 70 75 80

Asp Leu Ser Phe Lys Lys Gly Glu Lys Met Lys Val Leu Glu Glu His
 85 90 95

Gly Glu Trp Trp Lys Ala Lys Ser Leu Leu Thr Lys Lys Glu Gly Phe
 100 105 110

Ile Pro Ser Asn Tyr Val Ala Lys Leu Asn Thr Leu Glu Thr Glu Glu
 115 120 125

Trp Phe Phe Lys Asp Ile Thr Arg Lys Asp Ala Glu Arg Gln Leu Leu
 130 135 140
 Ala Pro Gly Asn Ser Ala Gly Ala Phe Leu Ile Arg Glu Ser Glu Thr
 145 150 155 160
 Leu Lys Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Pro Val His
 165 170 175
 Gly Asp Val Ile Lys His Tyr Lys Ile Arg Ser Leu Asp Asn Gly Gly
 180 185 190
 Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Cys Ile Ser Asp Met Ile
 195 200 205
 Lys His Tyr Gln Lys Gln Ala Asp Gly Leu Cys Arg Arg Leu Glu Lys
 210 215 220
 Ala Cys Ile Ser Pro Lys Pro Gln Lys Pro Trp Asp Lys Asp Ala Trp
 225 230 235 240
 Glu Ile Pro Arg Glu Ser Ile Lys Leu Val Lys Arg Leu Gly Ala Gly
 245 250 255
 Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Asn Asn Ser Thr Lys Val
 260 265 270
 Ala Val Lys Thr Leu Lys Pro Gly Thr Met Ser Val Gln Ala Phe Leu
 275 280 285
 Glu Glu Ala Asn Leu Met Lys Thr Leu Gln His Asp Lys Leu Val Arg
 290 295 300
 Leu Tyr Ala Val Val Thr Arg Glu Glu Pro Ile Tyr Ile Ile Thr Glu
 305 310 315 320
 Tyr Met Ala Lys Gly Ser Leu Leu Asp Phe Leu Lys Ser Asp Glu Gly
 325 330 335
 Gly Lys Val Leu Leu Pro Lys Leu Ile Asp Phe Ser Ala Gln Ile Ala
 340 345 350
 Glu Gly Met Ala Tyr Ile Glu Arg Lys Asn Tyr Ile His Arg Asp Leu
 355 360 365
 Arg Ala Ala Asn Val Leu Val Ser Glu Ser Leu Met Cys Lys Ile Ala
 370 375 380
 Asp Phe Gly Leu Ala Arg Val Ile Glu Asp Asn Glu Tyr Thr Ala Arg
 385 390 395 400
 Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn
 405 410 415
 Phe Gly Cys Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu
 420 425 430

Leu Tyr Glu Ile Val Thr Tyr Gly Lys Ile Pro Tyr Pro Gly Arg Thr
 435 440 445

Asn Ala Asp Val Met Thr Ala Leu Ser Gln Gly Tyr Arg Met Pro Arg
 450 455 460

Val Glu Asn Cys Pro Asp Glu Leu Tyr Asp Ile Met Lys Met Cys Trp
 465 470 475 480

Lys Glu Lys Ala Glu Glu Arg Pro Thr Phe Asp Tyr Leu Gln Ser Val
 485 490 495

Leu Asp Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Gln Gln Gln Pro
 500 505 510

<210> 17

<211> 505

<212> PRT

<213> Homo sapiens

<400> 17

Met Gly Ser Met Lys Ser Lys Phe Leu Gln Val Gly Gly Asn Thr Phe
 1 5 10 15

Ser Lys Thr Glu Thr Ser Ala Ser Pro His Cys Pro Val Tyr Val Pro
 20 25 30

Asp Pro Thr Ser Thr Ile Lys Pro Gly Pro Asn Ser His Asn Ser Asn
 35 40 45

Thr Pro Gly Ile Arg Glu Ala Gly Ser Glu Asp Ile Ile Val Val Ala
 50 55 60

Leu Tyr Asp Tyr Glu Ala Ile His His Glu Asp Leu Ser Phe Gln Lys
 65 70 75 80

Gly Asp Gln Met Val Val Leu Glu Glu Ser Gly Glu Trp Trp Lys Ala
 85 90 95

Arg Ser Leu Ala Thr Arg Lys Glu Gly Tyr Ile Pro Ser Asn Tyr Val
 100 105 110

Ala Arg Val Asp Ser Leu Glu Thr Glu Glu Trp Phe Phe Lys Gly Ile
 115 120 125

Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro Gly Asn Met Leu
 130 135 140

Gly Ser Phe Met Ile Arg Asp Ser Glu Thr Thr Lys Gly Ser Tyr Ser
 145 150 155 160

Leu Ser Val Arg Asp Tyr Asp Pro Arg Gln Gly Asp Thr Val Lys His
 165 170 175

Tyr Lys Ile Arg Thr Leu Asp Asn Gly Gly Phe Tyr Ile Ser Pro Arg
 180 185 190

Ser Thr Phe Ser Thr Leu Gln Glu Leu Val Asp His Tyr Lys Lys Gly
 195 200 205

Asn Asp Gly Leu Cys Gln Lys Leu Ser Val Pro Cys Met Ser Ser Lys
 210 215 220

Pro Gln Lys Pro Trp Glu Lys Asp Ala Trp Glu Ile Pro Arg Glu Ser
 225 230 235 240

Leu Lys Leu Glu Lys Lys Leu Gly Ala Gly Gln Phe Gly Glu Val Trp
 245 250 255

Met Ala Thr Tyr Asn Lys His Thr Lys Val Ala Val Lys Thr Met Lys
 260 265 270

Pro Gly Ser Met Ser Val Glu Ala Phe Leu Ala Glu Ala Asn Val Met
 275 280 285

Lys Thr Leu Gln His Asp Lys Leu Val Lys Leu His Ala Val Val Thr
 290 295 300

Lys Glu Pro Ile Tyr Ile Ile Thr Glu Phe Met Ala Lys Gly Ser Leu
 305 310 315 320

Leu Asp Phe Leu Lys Ser Asp Glu Gly Ser Lys Gln Pro Leu Pro Lys
 325 330 335

Leu Ile Asp Phe Ser Ala Gln Ile Ala Glu Gly Met Ala Phe Ile Glu
 340 345 350

Gln Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala Asn Ile Leu Val
 355 360 365

Ser Ala Ser Leu Val Cys Lys Ile Ala Asp Phe Gly Leu Ala Arg Val
 370 375 380

Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala Lys Phe Pro Ile
 385 390 395 400

Lys Trp Thr Ala Pro Glu Ala Ile Asn Phe Gly Ser Phe Thr Ile Lys
 405 410 415

Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Met Glu Ile Val Thr Tyr
 420 425 430

Gly Arg Ile Pro Tyr Pro Gly Met Ser Asn Pro Glu Val Ile Arg Ala
 435 440 445

Leu Glu Arg Gly Tyr Arg Met Pro Arg Pro Glu Asn Cys Pro Glu Glu
 450 455 460

Leu Tyr Asn Ile Met Met Arg Cys Trp Lys Asn Arg Pro Glu Glu Arg
 465 470 475 480

Pro Thr Phe Glu Tyr Ile Gln Ser Val Leu Asp Asp Phe Tyr Thr Ala
 485 490 495

Thr Glu Ser Gln Tyr Gln Gln Gln Pro
500 505

<210> 18
<211> 509
<212> PRT
<213> Homo sapiens

<400> 18
Met Gly Cys Gly Cys Ser Ser His Pro Glu Asp Asp Trp Met Glu Asn
1 5 10 15

Ile Asp Val Cys Glu Asn Cys His Tyr Pro Ile Val Pro Leu Asp Gly
20 25 30

Lys Gly Thr Leu Leu Ile Arg Asn Gly Ser Glu Val Arg Asp Pro Leu
35 40 45

Val Thr Tyr Glu Gly Ser Asn Pro Pro Ala Ser Pro Leu Gln Asp Asn
50 55 60

Leu Val Ile Ala Leu His Ser Tyr Glu Pro Ser His Asp Gly Asp Leu
65 70 75 80

Gly Phe Glu Lys Gly Glu Gln Leu Arg Ile Leu Glu Gln Ser Gly Glu
85 90 95

Trp Trp Lys Ala Gln Ser Leu Thr Thr Gly Gln Glu Gly Phe Ile Pro
100 105 110

Phe Asn Phe Val Ala Lys Ala Asn Ser Leu Glu Pro Glu Pro Trp Phe
115 120 125

Phe Lys Asn Leu Ser Arg Lys Asp Ala Glu Arg Gln Leu Leu Ala Pro
130 135 140

Gly Asn Thr His Gly Ser Phe Leu Ile Arg Glu Ser Glu Ser Thr Ala
145 150 155 160

Gly Ser Phe Ser Leu Ser Val Arg Asp Phe Asp Gln Asn Gln Gly Glu
165 170 175

Val Val Lys His Tyr Lys Ile Arg Asn Leu Asp Asn Gly Gly Phe Tyr
180 185 190

Ile Ser Pro Arg Ile Thr Phe Pro Gly Leu His Glu Leu Val Arg His
195 200 205

Tyr Thr Asn Ala Ser Asp Gly Leu Cys Thr Arg Leu Ser Arg Pro Cys
210 215 220

Gln Thr Gln Lys Pro Gln Lys Pro Trp Trp Glu Asp Glu Trp Glu Val
225 230 235 240

Pro Arg Glu Thr Leu Lys Leu Val Glu Arg Leu Gly Ala Gly Gln Phe
245 250 255

Gly Glu Val Trp Met Gly Tyr Tyr Asn Gly His Thr Lys Val Ala Val
 260 265 270
 Lys Ser Leu Lys Gln Gly Ser Met Ser Pro Asp Ala Phe Leu Ala Glu
 275 280 285
 Ala Asn Leu Met Lys Gln Leu Gln His Gln Arg Leu Val Arg Leu Tyr
 290 295 300
 Ala Val Val Thr Gln Glu Pro Ile Tyr Ile Ile Thr Glu Tyr Met Glu
 305 310 315 320
 Asn Gly Ser Leu Val Asp Phe Leu Lys Thr Pro Ser Gly Ile Lys Leu
 325 330 335
 Thr Ile Asn Lys Leu Leu Asp Met Ala Ala Gln Ile Ala Glu Gly Met
 340 345 350
 Ala Phe Ile Glu Glu Arg Asn Tyr Ile His Arg Asp Leu Arg Ala Ala
 355 360 365
 Asn Ile Leu Val Ser Asp Thr Leu Ser Cys Lys Ile Ala Asp Phe Gly
 370 375 380
 Leu Ala Arg Leu Ile Glu Asp Asn Glu Tyr Thr Ala Arg Glu Gly Ala
 385 390 395 400
 Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala Ile Asn Tyr Gly Thr
 405 410 415
 Phe Thr Ile Lys Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Thr Glu
 420 425 430
 Ile Val Thr His Gly Arg Ile Pro Tyr Pro Gly Met Thr Asn Pro Glu
 435 440 445
 Val Ile Gln Asn Leu Glu Arg Gly Tyr Arg Met Val Arg Pro Asp Asn
 450 455 460
 Cys Pro Glu Glu Leu Tyr Gln Leu Met Arg Leu Cys Trp Lys Glu Arg
 465 470 475 480
 Pro Glu Asp Arg Pro Thr Phe Asp Tyr Leu Arg Ser Val Leu Glu Asp
 485 490 495
 Phe Phe Thr Ala Thr Glu Gly Gln Tyr Gln Pro Gln Pro
 500 505

<210> 19
 <211> 499
 <212> PRT
 <213> Mus sp.

<400> 19
 Met Gly Leu Leu Ser Ser Lys Arg Gln Val Ser Glu Lys Gly Lys Gly
 1 5 10 15

Trp Ser Pro Val Lys Ile Arg Thr Gln Asp Lys Ala Pro Pro Pro Leu
 20 25 30

Pro Pro Leu Val Val Phe Asn His Leu Ala Pro Pro Ser Pro Asn Gln
 35 40 45

Asp Pro Asp Glu Glu Glu Arg Phe Val Val Ala Leu Phe Asp Tyr Ala
 50 55 60

Ala Val Asn Asp Arg Asp Leu Gln Val Leu Lys Gly Glu Lys Leu Gln
 65 70 75 80

Val Leu Arg Ser Thr Gly Asp Trp Trp Leu Ala Arg Ser Leu Val Thr
 85 90 95

Gly Arg Glu Gly Tyr Val Pro Ser Asn Phe Val Ala Pro Val Glu Thr
 100 105 110

Leu Glu Val Glu Lys Trp Phe Phe Arg Thr Ile Ser Arg Lys Asp Ala
 115 120 125

Glu Arg Gln Leu Leu Ala Pro Met Asn Lys Ala Gly Ser Phe Leu Ile
 130 135 140

Arg Glu Ser Glu Ser Asn Lys Gly Ala Phe Ser Leu Ser Val Lys Asp
 145 150 155 160

Ile Thr Thr Gln Gly Glu Val Val Lys His Tyr Lys Ile Arg Ser Leu
 165 170 175

Asp Asn Gly Gly Tyr Tyr Ile Ser Pro Arg Ile Thr Phe Pro Thr Leu
 180 185 190

Gln Ala Leu Val Gln His Tyr Ser Lys Lys Gly Asp Gly Leu Cys Gln
 195 200 205

Lys Leu Thr Leu Pro Cys Val Asn Leu Ala Pro Lys Asn Leu Trp Ala
 210 215 220

Gln Asp Glu Trp Glu Ile Pro Arg Gln Ser Leu Lys Leu Val Arg Lys
 225 230 235 240

Leu Gly Ser Gly Gln Phe Gly Glu Val Trp Met Gly Tyr Tyr Lys Asn
 245 250 255

Asn Met Lys Val Ala Ile Lys Thr Leu Lys Glu Gly Thr Met Ser Pro
 260 265 270

Glu Ala Phe Leu Gly Glu Ala Asn Val Met Lys Thr Leu Gln His Glu
 275 280 285

Arg Leu Val Arg Leu Tyr Ala Val Val Thr Arg Glu Pro Ile Tyr Ile
 290 295 300

Val Thr Glu Tyr Met Ala Arg Gly Cys Leu Leu Asp Phe Leu Lys Thr
 305 310 315 320

Asp Glu Gly Ser Arg Leu Ser Leu Pro Arg Leu Ile Asp Met Ser Ala
 325 330 335

 Gln Val Ala Glu Gly Met Ala Tyr Ile Glu Arg Met Asn Ser Ile His
 340 345 350

 Arg Asp Leu Arg Ala Ala Asn Ile Leu Val Ser Glu Thr Leu Cys Cys
 355 360 365

 Lys Ile Ala Asp Phe Gly Leu Ala Arg Ile Ile Asp Ser Glu Tyr Thr
 370 375 380

 Ala Gln Glu Gly Ala Lys Phe Pro Ile Lys Trp Thr Ala Pro Glu Ala
 385 390 395 400

 Ile His Phe Gly Val Phe Thr Ile Lys Ala Asp Val Trp Ser Phe Gly
 405 410 415

 Val Leu Leu Met Val Ile Val Thr Tyr Gly Arg Val Pro Tyr Pro Gly
 420 425 430

 Met Ser Asn Pro Glu Val Ile Arg Ser Leu Glu His Gly Tyr Arg Met
 435 440 445

 Pro Cys Pro Glu Thr Cys Pro Pro Glu Leu Tyr Asn Asp Ile Ile Thr
 450 455 460

 Glu Cys Trp Arg Gly Arg Pro Glu Glu Arg Pro Thr Phe Glu Phe Leu
 465 470 475 480

 Gln Ser Val Leu Glu Asp Phe Tyr Thr Ala Thr Glu Gly Gln Tyr Glu
 485 490 495

 Leu Gln Pro

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<210> 20
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (14)
<223> A, T, C, G, other or unknown

<220>
<221> modified_base
<222> (20)
<223> A, T, C, G, other or unknown

<220>
<221> modified_base
<222> (23)
<223> A, T, C, G, other or unknown

<220>
<221> modified_base

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<222> (26)
<223> A, T, C, G, other or unknown

<220>
<223> Description of Artificial Sequence: Primer

<400> 20
ggaattccca ymgnrraytn rcnrcnmg                                28

<210> 21
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<221> modified_base
<222> (12)
<223> A, T, C, G, other or unknown

<220>
<221> modified_base
<222> (18)
<223> A, T, C, G, other or unknown

<220>
<221> modified_base
<222> (24)
<223> A, T, C, G, other or unknown

<220>
<223> Description of Artificial Sequence: Primer

<400> 21
ggaattccrw rnswccanac stcnsa                                26

<210> 22
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide

<400> 22
Gly Gln Asp Ala Asp Gly Ser Thr Ser Pro Arg Ser Gln Glu Pro
     1           5           10          15

<210> 23
<211> 16
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence: Synthetic peptide

<400> 23
Gln Gln Leu Leu Ser Ser Ile Glu Pro Leu Arg Glu Lys Asp Lys His
1 5 10 15

<210> 24
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Illustrative peptide

a¹⁴
cont

<220>
<221> MOD_RES
<222> (6)
<223> Variable amino acid

<400> 24
Ser Asp Val Trp Ser Xaa
1 5